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Variability and Diversity Studies Using Morpho-physiological Traits in Wheat (*Triticum aestivum* L.) under Irrigated and Rainfed Conditions

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ABSTRACT

A study was conducted at Rice and Wheat Research Centre, Malan and Department of Genetics and Plant Breeding, CSK HPKV, Palampur, Himachal Pradesh, India during October, 2013 to May, 2014 to identify traits for developing reliable selection criteria and conduct diversity analysis. In the present investigation, fifty-six diverse wheat genotypes were evaluated in an alpha-design using various yield attributes and drought indices under irrigated and moisture-stress environments over three environments in two locations. Results from the study indicated significant differences for almost all the traits under all three environments and pooled environments. Variability studies showed high phenotypic and genotypic coefficient of variability with high heritability coupled with high genetic advance for seedling vigour under irrigated conditions as well as under moisture-stress conditions along with membrane stability index, dry matter accumulation and grain yield. On the basis of low DSI and high DRI values and relative ranking of morpho-physiological traits, seven genotypes HPW 368, NI 5439, CM 33, CM 19, HPW 236, CM 11 and HPW 349 have been found to be moisture-stress tolerant. Association studies showed that grains spike^{-1}, harvest index, thousand grain weight, excised leaf water loss and days to 75% maturity are most important traits for selection of tolerant genotypes. On the basis of D^2 statistics, 56 genotypes were grouped into twelve main clusters and genotypes HPW 277, HPW 297 and NIAW 1415 were found superior as well as diverse for most of the traits. Hence, these genotypes can be used in breeding programmes aimed at enhancing drought tolerance.

KEYWORDS: DSI, DRI, diversity, moisture-stress, variability, wheat

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1. INTRODUCTION

Wheat is one of the most important staple food crops in the world and considered as 'king of cereals', as it feeds more than 36% of the global population. Globally, it is grown in 222.17 mha area with production of 779.9 mt (Anonymous, 2023). In India, it ranks second among cereals with an area of 31.13 mha and production of 106.84 mt (Anonymous, 2022). Food production throughout the world is affected by several biotic and abiotic stresses. Among abiotic stresses, moisture-stress is one such significant environmental stress in agriculture which limits plant growth and field crops production (Delahunty et al., 2015; Wang et al., 2017; Sallam et al., 2019; Khadka et al., 2020; Ahmad et al., 2022). Wheat has potential sensitivity to water stress especially during its reproductive stage (Chowdhury et al., 2021). Hence, the reduction of grain yield in wheat under moisture-stress is one of the primary concerns of the wheat breeding programme throughout the world (Allahverdiyev et al., 2015; Liu and Hwang, 2015; Ahmed et al., 2020). Drought tolerance of wheat is a complex trait with multifactorial determination, depending on interactions of genotypes and environmental conditions (Mwadzingeni et al., 2016). However, development of drought tolerant genotypes is limited by low heritability for drought resistance and lack of simple and effective selection strategies (Semahegn et al., 2021; Kumar et al., 2023). Therefore, identification of drought tolerance mechanisms and availability of simple and reliable selection criteria are of great significance for development of drought resistant cultivars (Ahmed et al., 2019; Pour-Aboughadareh et al., 2020; Cai et al., 2020; Langridge and Reynolds et al., 2021).

To meet the increasing demand of wheat production without increasing area, there is need to incorporate new physiological tools (Abid et al., 2018). These traits will contribute to more objective screening/selection for yield in early generations when grain yield may not be properly assessed. At present, the best indicator of drought tolerance used in wheat breeding programme is Drought Susceptibility Index (DSI) (Fischer and Maurer, 1978). This index, however, considers neither the confounding effects of flowering time on yield nor the effects of yield potential on grain yield under drought stress (Arraudeau, 1989). Bidinger et al. (1987) proposed a Drought Response Index (DRI) which is based on residual variation in grain yield adjusted for experimental error. This method is based on multiple regression technique which is capable of removing the influence of intervening variables, namely, influence of early heading and high yield potential under drought stress conditions (Aberkane et al., 2021; Haque et al., 2021). DRI has been considered as the best selection criterion for evaluation of drought resistant cultivars (Eid and Sabry, 2019).

Wheat production can be enhanced through the development of improved cultivars with wider genetic base and capable of producing better yield under various agro-climatic conditions. Evaluation of genetic diversity levels among adapted elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development (Bapela et al., 2022). Further, the utilization of physiological information requires establishment of association between plant productivity under stress and various possible physiological components of drought tolerance. So, understanding of physiological mechanisms that enable plants to adapt to water deficit and maintain growth and productivity during stress period can help in screening and selection of drought tolerant genotypes (Mohammadi, 2018; Gupta et al., 2020). In view of all these facts, the objectives of present investigation were to screen diverse wheat genotypes for moisture-stress tolerance and associated morpho-physiological traits, conduct diversity analysis of genotypes and select important traits to be used as parameters for identifying tolerant wheat genotypes.

2. MATERIALS AND METHODS

2.1. Plant material and site

The experimental material comprised of fifty-six genetically diverse wheat genotypes which included lines from CIMMYT rainfed wheat improvement programme, some pre-released improved lines, released varieties and landrace. The details of the material use in the study is mentioned in Table 1. These genotypes were evaluated both under moisture-stress (rainfed) and non-stress (irrigated) conditions during October-May, 2013–14 at Rice and Wheat Research Centre (RWRC), Malan and under moisture-stress conditions at Department of Genetics and Plant Breeding, CSK HPKV, Palampur, Himachal Pradesh, India.

2.2. Experimental procedure

These wheat genotypes were evaluated in α-design with three replications under both non-stress (irrigated) environment (E_1) and under rainfed (moisture-stress) environment (E_2) under field conditions at RWRC, Malan (elevation of about 950 m a.m.s.l. having 32°1' latitude and 76°2' longitude) and only under rainfed environment (E_3) at Department of Genetics and Plant Breeding, CSK HPKV, Palampur (1290.8 m a.m.s.l. having latitude 32°6' N and longitude 76°3' E). Each genotype was grown in 2×0.40 m^2 plot with row to row spacing of 20 cm. Standard agronomic practices were followed to raise the crop under both the sites. Observations were recorded based on five competitive plants selected randomly in each replication under E_1, E_2 and E_3 conditions. Various physiological, agro-morphological and phenological traits such as seedling vigour (SV), flag leaf area (FLA), plant height (PH), excised leaf water loss (ELWL), stem reserve mobilization (SRM), membrane stability index (MSI), dry matter accumulation (DMA), tillers plant^{-1} (TPP), grains spike^{-1} (GPS), 1000-grain weight (TGW), biological yield plant^{-1} (BYP), grain yield plant^{-1} (GYP), harvest index (HI) and phenological traits such as days to 50% flowering (DTF50) and days to 75% maturity (D75M) were recorded. The equations used for calculating these parameters is mentioned below.

ELWL (%)=[FW-Weight after 6 hours/FW-DW]× 100 ……(1)

where FW: Fresh weight and DW: Dry weight

SRM=Grain yield plant^{-1}/Dry stem weight ……(2)

Injury (%)=$[1-\{(1-T_1/T_2)/(1-T_1/T_2)\}]\times100$ ……(3)

where T_1 and T_2 are the first and second conductivity measurements for the desiccation treatment, respectively. C_1 and C_2 are the first and second measurement of the control, respectively.

Besides, drought tolerance indices such as drought susceptibility index (DSI) was calculated from grain yield data recorded under non-stress (E_1) and moisture-stress (E_2) environments as per Fischer and Maurer (1978) and drought response index (DRI) was computed for an individual genotype as per Bidinger et al. (1987).

DSI=$\{1-(Y_d/Y_p)\}$ / D……………(4)

D=1-(Mean Y_d of all the genotypes/Mean Y_p of all genotypes)……………(5)

where, Y_d is the mean grain yield of a genotype under moisture-stress environment, Y_p is the mean grain yield under non-stress environment and D is the drought intensity.

DRI=1-(Y_a-Y_{est})/SES……………(6)

where, Y_{est} and Y_a are the yields of the cultivars to be estimated by regression and actual yield under stress, respectively and SES is the standard error of multiple regression.

2.3. *Statistical analysis*

The observations recorded were statistically analyzed as per procedure of α-Design by following the model given by Parsad et al. (2007). The analysis was performed using PROC GLM of SAS software. All possible pair wise treatment comparisons were performed using LSMEANS statement of PROC GLM. Estimates of variability such as genotypic, phenotypic and environmental coefficients of variation were calculated along with heritability in broad sense (h^2_{bs}) and genetic advance as per Burton and De Vane (1953) and Johnson et al. (1955) (Table 1).

Table 1: Details of the plant material used in the investigation

Sl. No.	Genotype	Pedigree	Source
1.	CM 42	MILAN/SHA7/3/THB/CEP7780//SHA4/LIRA/4/SHA4/CHIL	CIMMYT rain-fed wheat improvement programme
2.	CM 15	SOKOLL/WBLL1	
3.	CM 41	MUNAL #1	
4.	CM 11	TC870344/GUI//TEMPORALERA M 87/AGR/3/2*WBLL1	
5.	CM 33	ATTILA/BAV92//PASTOR	
6.	CM 26	SOKOLL/92.001E7.32.5	
7.	CM 2	BERKUT	
8.	CM 20	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN	
9.	CM 39	KINGBIRD	
10.	CM 10	BABAX/LR42//BABAX/3/ER2000	
11.	CM 19	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	
12.	CM 27	SOKOLL/EXCALIBUR	
13.	CM 16	PASTOR//HXL7573/2*BAU/3/WBLL1	
14.	CM 17	SOKOLL/3/PASTOR//HXL7573/2*BAU	
15.	CM 29	BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA(224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	
16.	CM 43	SHORTENED SR26 TRANSLOCATION	
17.	CM 18	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1	

Table 1: Continue...

Sl. No.	Genotype	Pedigree	Source
18.	CM 24	MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	
19.	CM 23	SOKOLL//SUNCO/2*PASTOR	
20.	CM 32 (C)	Vorobey	
21.	HPW 327	EBWYT 518	RWRC, Malan
22.	HPW 280	SHA7/VEE#5/5/VEE#8//JUP/BJY/3/F3/F3.71/TRM/4/CMSS96M022183-050M-040Y-0100M-020Y-14M-0Y	
23.	HPW 269	PRL/2*PASTOR	
24.	HPW 292	TRAP# 1/BOW//PFAV/3/MALAN	
25.	HPW 147	DOM 50	
26.	HPW 376	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*/PASTOR	
27.	HPW 281	PW351 × HPW 89-P1	
28.	HPW 301	W462/VEE/KOEL	
29.	HPW 277	CPAN 3063/HS 295-P2	
30.	HPW 302	SN 1/2*PASTOR	
31.	HPW 334	EIGN M1 YCSN-31 (2007-08)	
32.	HPW 236	WL 711/PGS 990/VL 780	
33.	HPW 368	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR	
34.	HPW 299	VHW 3574 DWR-WS 18-2	
35.	HPW 155	BT 2549/FATH	
36.	HPW 297	CPAN1922/HS 295	
37.	HPW 349	OASIS/SKAUZ//4**BCN/3/PASTOR/4/KAUZ	
38.	HPW 89 (C)	INTERMEDIO RODI / HD 2248	
39.	HD 2888	C 306 / T. sphaerococcum//HW 2004	IARI, New Delhi
40.	WR 544	KALYANSONA/HD 1999//HD2204/3/DW 38	
41.	HS 507	KAUZ/MYNA/VUL//BUC/FLK/4/MILAN	
42.	HS 490	HS 364/HPW 114//HS240/HS 346	
43.	HW 2004	C 306*7//TR 380-14#7/3 AG 14	IARI, RS, Wellington
44.	Bhalyani collection	Farmers' variety	Bhalyani Kullu
45.	VL 907	DYBR 1982-83/842 ABVD 50/VW 9365//PBW 343	VPKAS, Almora
46.	VL 892	WH 542/PBW 226	
47.	C 306 (C)	REGENT1974/3*CHZ//*2C591/3/P19/C 281	CCS HAU, Hisar
48.	WH 1021	NYOT 95/SONAK	
49.	Kanku	Local Landrace	Farmers
50.	PBW 550	WH 594/RAJ 3856/W 485	PAU, Ludhiana
51.	NI5439	NI 8883/MP 1055	MPKV, Niphad
52.	NIAW 34	CNO 79/PRL "S"	
53.	NIAW 1689	LOK 45/NIAW 34	

Table 1: Continue...

Sl. No.	Genotype	Pedigree	Source
54.	NIAW 1415	GW 9506/PRL//PRL	
55.	DPW 621-50	KAUZ/ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	PAU- IIWBR
56.	DBW 17	CMH 79A. 95/3*CN 079//RAJ 3777	IIWBR, Karnal

3. RESULTS AND DISCUSSION

3.1. *One way and pooled Analysis of variance (ANOVA) for three environments*

Analysis of variance for all the traits studied for three environments indicated significant mean squares differences due to genotypes for all the traits observed under irrigated (E1) and rainfed (E2 and E3) environments (Table 2). Earlier, Jatoi et al. (2012) and Kumar et al. (2023) reported similar significant results for all the yield and morpho-physiological traits in wheat. In a similar study by Rana et al. (2014), similar significant differences in genotypes for all the traits under study were found except for relative water content and ELWL.

Besides, combined analysis of variance pooled over three environments for all the traits except MSI has been given in Table 3. The mean squares for genotypes and genotypes ×environment interaction was found significant for all the characters which indicated the presence of variability among the genotypes and differential response of the strains/varieties under different environments. Recently, Abdolshahi et al. (2015) also reported considerable amount of genotypic variability for all the traits in both years under field and glass house experiments in wheat.

3.2. *Mean performance and variability parameters*

The mean performance and % of reduction in mean value for all the traits studied under stress is mentioned in Table 4. GY reduction under moisture-stress (E2 and E3) compared to irrigated conditions was found to be 43.32 and 39.8, respectively. The comparison of mean values of both the environments indicated that there was significant reduction of mean values under E2 as compared to E1 for almost all the traits. Reduction % of mean values under E2 environment over E1 environment was highest in GY (43.32) followed by SRM (35.78) and TGW (35.32). Reduction % of mean values under E3 environment over E1 environment was highest in GY (39.80) followed by TGW (35.30) and SV (30.00). TPP was the least affected (-18.63 and -22.00) character under both E2 and E3 environments. Significant reduction in GY and agro-morphological traits under moisture-stress conditions has been reported by many studies in wheat (Akram et al., 2010; Semahegn et al., 2020). Similar reduction in other trait performance under moisture stress as compared to irrigated conditions has been mentioned in Table 4. Zhang et al. (2006) observed that GPS was reduced more relative to other yield components as stress severity increased and is the most important factor in determining GY under both irrigated and non-irrigated conditions.

A wide range of variation was observed among different wheat genotypes with regard to different characters studied in three environments. The estimates of different parameters of variability along with mean and % of decrease in moisture-stress (E2 and E3) environment over irrigated (E1) environment are given in Table 4. PCV values of almost all traits were found to be closer to their corresponding GCV values, which indicated little effect of environmental variation on these traits. High PCV estimates (>30%) were found for SV and SRM in E1, SV, GY and MSI in E2 and SV, DMA and GY in E3 environment. Traits such as FLA, ELWL, TPP, GPS, TGW and BYP had moderate PCV estimates (15–30%) in all three environments whereas DMA and GY in E1, DMA and HI in E2, SRM and HI in E3 had moderate PCV estimates. Similarly, high GCV estimates were found for SV in E1, SV, MSI, GY in E2 and SV, DMA and GY in E3. Other traits viz., FLA, ELWL, SRM, TGW and BYP had moderate GCV estimates in both irrigated and rainfed environments whereas DMA and GY in E1, DMA, GPS and HI in E2, TPP, GPS and HI in E3 had moderate estimates. Moreover, for an effective selection programme, knowledge of the estimates of heritability and genetic advance is very useful and are important to obtain higher genetic gain. In our study, almost all traits had high heritability estimates (>80%) except TPP, GPS in E1, SRM, TPP and BYP in E2 and SRM and TPP in E3 which had moderate heritability estimates (50–80%) in both irrigated and rainfed conditions. Expected genetic advance as % of mean was found high (>50%) for SV and SRM in E1, SV, FLA, MSI, GY and HI in E2 and SV, DMA, GY and HI in E3. Moderate genetic advance estimates (25–50%) were found for ELWL, TGW and BYP in all three environments whereas FLA, DMA, TPP, GY and HI in E1, SRM, DMA and GPS in E2 and FLA, SRM, TPP and GPS in E3 had moderate estimates of genetic advance. Rest of the traits such as PH, DTF50 and D75M showed low PCV, GCV, heritability and genetic advance estimates in all the three environments. High heritability coupled with high genetic advance was found for SV and SRM in E1, SV, FLA, MSI, GY and HI in E2 and SV, DMA, GY and HI in E3 whereas moderate heritability coupled with moderate genetic advance was observed for FLA, ELWL,

Table 2: Analysis of variance of wheat genotypes for different traits observed under irrigated (E_1) and rainfed (E_2 and E_3) environments

Traits/source	Mean sum of squares				
	Environment	Replication	Blocks within replication	Genotypes	Error
d.f.		2	18	55	92
SV	E_1	2.28	2.19	55.00*	1.56
	E_2	2.28	0.34	32.27*	0.41
	E_3	0.42	1.02	30.50*	0.88
FLA (cm^2)	E_1	2.53	2.19	54.99*	1.57
	E_2	2.27	0.32	32.35*	0.34
	E_3	0.69	0.83	30.68*	0.77
PH (cm)	E_1	0.30	0.27	165.23*	0.54
	E_2	2.58	7.95	140.35*	7.85
	E_3	0.65	4.05	131.55*	3.47
ELWL (%)	E_1	21.31	4.20	168.12*	5.19
	E_2	15.63	4.78	180.72*	5.02
	E_3	15.67	4.54	191.08*	4.32
SRM	E_1	2.03	3.36	191.43*	3.18
	E_2	6.45	2.03	104.67*	3.13
	E_3	4.51	2.25	127.00*	1.59
MSI (%)	E_1	-	-	-	-
	E_2	18.60	1.24	80.22*	0.91
	E_3	-	-	-	-
DMA (g)	E_1	1.619	0.48	12.42*	0.30
	E_2	7.31	1.17	10.38*	0.79
	E_3	4.08	0.12	15.86*	0.30
TPP	E_1	0.02	0.78	0.59*	0.07
	E_2	0.01	0.22	0.82*	0.12
	E_3	0.55	0.14	0.99*	0.12
GPS	E_1	20.53	5.06	201.99*	4.09
	E_2	7.51	10.99	193.92*	9.96
	E_3	0.03	2.67	221.72*	3.36
TGW (g)	E_1	2.64	1.35	161.53*	1.76
	E_2	2.28	0.54	146.02*	1.24
	E_3	0.38	2.00	138.31*	1.92
BYP (g)	E_1	2.14	0.95	23.19*	0.70
	E_2	23.94	2.62	14.45*	1.96
	E_3	6.34	0.48	20.35*	0.89
GY (g)	E_1	0.25	0.22	5.81*	0.15
	E_2	1.91	0.24	3.69*	0.18
	E_3	1.16	0.07	4.04*	0.13

Table 2: Continue...

Traits/source	Mean sum of squares				
	Environment	Replication	Blocks within replication	Genotypes	Error
d.f.		2	18	55	92
HI (%)	E_1	1.88	1.89	88.27*	1.77
	E_2	0.69	0.87	161.83*	1.87
	E_3	5.58	1.08	157.59*	0.91
DTF50	E_1	0.79	0.70	12.93*	0.81
	E_2	7.05	1.11	10.45*	0.74
	E_3	4.13	0.12	15.88*	0.29
D75M	E_1	6.60	28.79	73.42*	28.73
	E_2	4.17	2.07	44.72*	3.95
	E_3	2.92	2.19	36.53*	3.29

* $p<0.05$

Table 3: Pooled analysis of variance of wheat genotypes for different traits over three environments

Traits/ Source	Mean sum of squares					
	Environment (Env)	Replication (Env)	Block (Env*Rep)	Genotypes (Gen)	(Gen*Env)	Error
d.f.	2	6	54	55	110	276
SV	1011.24	1.73	1.26	101.12*	11.54*	0.97
FLA (cm^2)	1043.5	1.83	1.11	98.45*	9.78*	0.90
PH (cm)	3373.67	1.18	4.09	311.54*	62.8*	3.95
ELWL (%)	1694.58	17.54	4.51	481.07*	29.43*	4.85
SRM	10143.99	4.33	2.55	57.35*	132.88*	2.64
DMA (g)	28.59	0.19	0.059	0.58*	0.50*	0.06
TPP	22.23	0.19	0.57*	1.35*	0.52*	0.10
GPS	4487.72	9.36	6.24	331.86*	142.89*	5.80
TGW (g)	17577.52	1.77	1.3	355.09*	45.38*	1.64
BYP (g)	464.74	10.81	1.35	40.55*	8.72*	1.81
GY (g)	410.41	1.1	0.18	9.56*	1.99*	0.15
HI (%)	7283.6	2.72	1.28	258.89*	74.4*	1.52
DTF50	319.08	3.99	0.65	24.71*	7.28*	0.61
D75M	6569.48	3.68	11.01	79.49*	37.58*	11.99

*$p<0.05$

DMA, TGW, BYP, GY and HI in E1, ELWL, DMA, GPS and TGW in E2 and FLA, ELWL, GPS, TGW and BYP in E3. Similar high heritability coupled with high genetic advance for GY been reported (Chandra et al., 2010; Yadav et al., 2014; Kumar et al., 2023; Rana et al., 2023). High heritability and high genetic advance for these traits indicated additive genetic control suggesting that early generation phenotypic selection would be effective of these traits under both the environments. Besides, high heritability and genetic advance, MSI appeared to be controlled mainly by additive gene action which indicated that this trait can be used as an effective selection criterion for selection of tolerant genotypes under stress conditions. However, contrary to these results, membrane stability index was reported to be controlled by non-additive gene action by Yildrim et al. (2009).

3.3. Relative drought tolerance/ranking of wheat genotypes

The relative drought tolerance of genotypes under study was assessed by two indices viz. Drought Susceptibility Index

Table 4: Range, mean and variability parameters for different characters under irrigated (E_1) and rainfed (E_2 and E_3) environments

Traits		Range	Mean±S.E.	% decrease under stress	ECV (%)	GCV (%)	PCV (%)	h^2 (bs) (%)	G.A. (%)
SV	E_1	8.48–28.39	14.91±0.77	-	8.97	31.04	32.31	92.3	61.43
	E_2	5.15–21.98	10.83±0.31	27.36	5.479	33.264	33.712	97.4	67.613
	E_3	5.65–22.55	10.44±0.51	30	8.472	33.633	34.684	94	67.186
FLA (cm^2)	E_1	22.66–53.42	35.42±1.08	-	5.28	22.13	22.75	94.6	44.33
	E_2	14.85–43.08	28.07±0.81	20.75	5.008	25.496	25.983	96.3	51.537
	E_3	15.45–43.79	27.88±1.09	21.28	6.775	24.795	25.704	93.1	49.271
PH (cm)	E_1	73.55–109.57	97.37±1.39	-	2.48	7.75	8.13	90.7	15.2
	E_2	66.80–108.50	92.41±1.29	5.09	2.415	8.558	8.892	92.6	16.967
	E_3	70.19–108.17	91.46±1.21	6.07	2.282	8.939	9.226	93.9	17.843
ELWL (%)	E_1	22.17–55.64	42.59±1.15	-	4.69	19.77	20.32	94.7	39.62
	E_2	15.22–37.93	27.64±0.93	35.1	5.819	22.578	23.316	93.8	45.039
	E_3	18.35–43.02	31.53±0.75	25.96	4.132	22.23	22.611	96.7	45.022
SRM	E_1	1.25–3.78	2.18±0.17	-	13.32	28.45	31.41	82	53.07
	E_2	0.74–2.34	1.40±0.12	35.78	15.353	21.546	26.457	66.3	36.147
	E_3	1.04–2.55	1.55±0.12	28.84	13.085	22.27	25.83	74.3	39.555
MSI (%)	E_1	-	-	-	-	-	-	-	-
	E_2	2.54–25.76	13.03±0.54	-	7.125	41.034	41.647	97.1	83.283
	E_3	-	-	-	-	-	-	-	-
DMA (g)	E_1	6.57 –16.14	10.55±0.53	-	8.66	20.03	21.82	84.2	37.88
	E_2	4,44–13.92	8.11±0.52	23.13	11.051	23.976	26.401	82.5	44.856
	E_3	3,49–13.22	8.24±0.30	21.9	6.225	30.402	31.032	96	61.355
TPP	E_1	2.13–4.27	3.06±0.16	-	8.85	14.46	16.95	72.8	25.42
	E_2	2.50–5.10	3.63±0.21	-18.63	10.323	14.432	17.744	66.2	24.181
	E_3	2.40–5.13	3.73±0.20	-22.00	9.314	16.018	18.529	74.7	28.525
GPS	E_1	36.20–71.03	54.51±3.41	-	10.84	13.38	17.22	60.4	21.42
	E_2	31.13–65.73	45.56±1.90	16.42	4.18	18.314	18.785	95	36.78
	E_3	30.33–65.80	47.29±0.89	13.25	3.259	19.242	19.516	97.2	39.082
TGW (g)	E_1	36.32–66.44	50.20±0.75	-	2.57	15.64	15.85	97.4	31.8
	E_2	19.73–50.73	32.47±0.61	35.32	3.252	23.627	23.85	98.1	48.217
	E_3	19.20–54.48	32.48±0.78	35.3	4.145	22.638	23.014	96.8	45.871
BYP (g)	E_1	10.69–25.95	15.92±0.51	-	5.59	18.17	19.01	91.4	35.79
	E_2	6.86–18.42	13.00±0.83	18.34	11.017	16.924	20.194	70.2	29.217
	E_3	7.76–21.70	13.14±0.52	17.45	6.899	20.917	22.025	90.2	40.92
GY (g)	E_1	3.87–12.37	6.51±0.23	-	6.15	23.17	23.98	93.4	46.14
	E_2	1.49–6.67	3.69±0.23	43.32	11.835	32.115	34.226	88	62.076
	E_3	1.95–7.06	3.92±0.20	39.8	8.73	32.039	33.208	93.1	63.68

Table 4: Continue...

Traits		Range	Mean±S.E.	% decrease under stress	ECV (%)	GCV (%)	PCV (%)	h^2 (bs) (%)	G.A. (%)
HI (%)	E_1	23.43–50.10	40.62±0.73	-	3.11	14.47	14.8	95.6	29.14
	E_2	12.74–47.13	28.55±0.73	29.71	4.456	27.997	28.349	97.5	56.957
	E_3	15.06–44.38	29.90±0.56	26.38	3.24	25.88	26.082	98.5	52.9
DTF50	E_1	108.00–125.67	116.01±0.95	-	1.42	3.43	3.71	85.3	6.52
	E_2	109.00–125.67	119.51±0.99	-3.02	1.435	3.254	3.556	83.7	6.134
	E_3	113.67–133.33	127.87±1.02	-10.22	1.379	2.775	3.099	80.2	5.119
D75M	E_1	152.00–169.67	160.45±0.97	-	1.05	2.98	3.16	89	5.78
	E_2	150.00–173.00	162.35±0.90	-1.18	0.959	3.729	3.85	93.8	7.44
	E_3	153.00–171.67	161.95±0.87	-0.93	0.929	3.459	3.582	93.3	6.882

(DSI) and Drought Response Index (DRI). The 'DSI' value for different wheat genotypes evaluated in the present study ranged from 0.03-1.64. Genotypes with low 'DSI' values (less than 1) can be considered to be drought resistant (Bruckner and Frohberg 1987), because they exhibited smaller yield reductions under water stress compared with well-watered conditions than the mean of all genotypes. Since lower value of DSI and higher value of DRI indicates greater drought resistance, some of the elite genotypes under study could be ear-marked as drought tolerant based on these two criteria. HPW 368 (0.03, 8.78) followed by NI 5439 (0.19, 8.45), CM 33 (0.25, 13.73), HPW 236 (0.37, 11.65), HPW 349 (0.45, 5.73), CM 19 (0.48, 10.98), CM 11 (0.48, 14.29), HS 490 (0.50, 5.84), HPW 297 (0.50, 12.51), HPW 269 (0.51, 10.36), HPW 302 (0.57, 6.20), CM 17 (0.59, 9.14), CM 29 (0.59, 6.96), NIAW 1415 (0.66, 7.14), HPW 155 (0.76, 4.15), HPW 281 (0.76, 1.84), VL 907 (0.77, 2.37), and WR 544 (0.86, 1.22) were found to be drought tolerant on the basis of low 'DSI' and higher DRI value (Figure 1). Ranking of these genotypes for other traits indicated that drought tolerance of NI 5439 may be attributed to high GY, TPP, GPS, lower ELWL and high SRM under stress environment. HPW 368 had high TPP, GPS, high HI and early maturing. Similarly, CM 33 had high GY, TPP, GPS, BYP, TGW, low ELWL, high DMA and early maturity under moisture-stress conditions. The drought tolerance of HPW 236 was attributable to high GY, TPP, TGW, HI, FLA, PH, low ELWL and earliness in maturity under stress conditions. CM 19 exhibited moisture-stress tolerance because of having good combination of high GY, GPS, HI, low ELWL and short maturity period. The moisture-stress tolerance of CM 11 may be attributed to high GY, GPS, TGW, BYP, HI, low ELWL and earliness in maturity. Besides, on the basis of high DSI and low DRI values, the

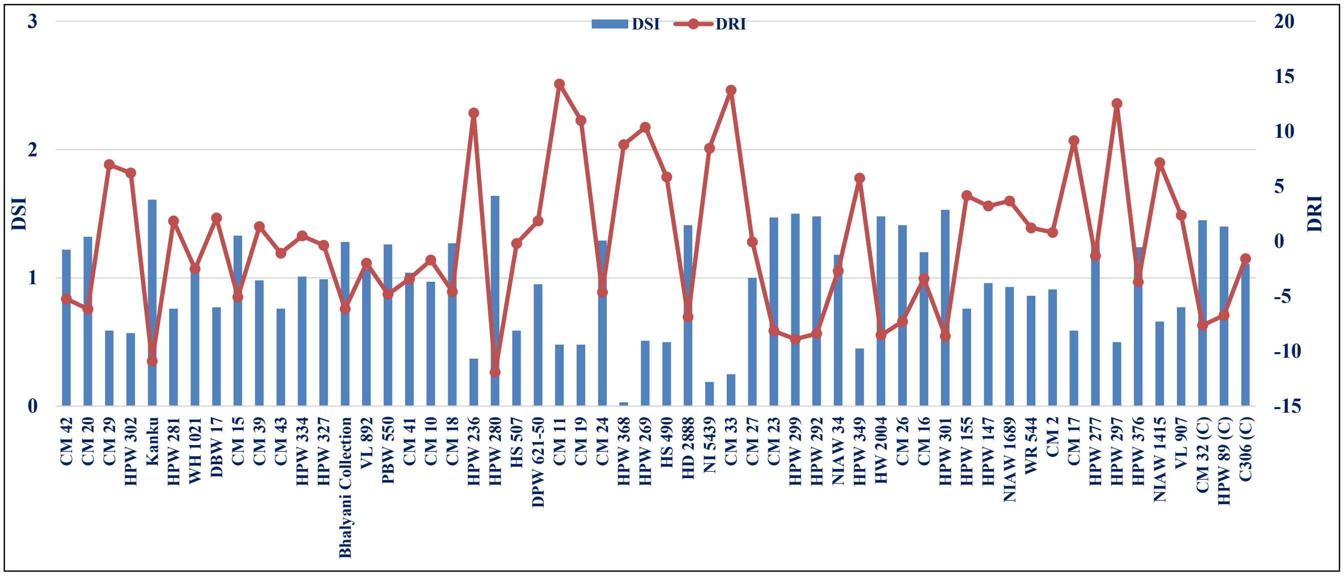

Figure 1: Variation in wheat genotypes for Drought Susceptibility Index (DSI) and Drought Response Index (DRI) values under rainfed environment (E_2)

wheat genotypes HPW 280 (1.64, -11.90), Kanku (1.61, -10.91), HPW 301 (1.53, -8.63), HPW 299 (1.50, -8.90), HPW 292 (1.48, -8.40), HW 2004 (1.48, -8.54) were categorised as the susceptible genotypes. Several workers have also highlighted drought resistant index (DRI) an important selection criterion for identifying high yielding genotypes in both conditions (Hu et al., 2007; Ashraf et al., 2015). Similar categorization of genotypes based on DSI was reported by Sharma et al. (2022).

3.4. Character association

Yield is a complex character and is a function of several component characters and their interaction with environment. Due to this fact, direct selection based on yield alone is not effective in crop improvement programmes. Therefore study of yield components and their inter-relationships is necessary. The pearson's correlation coefficients among different traits evaluated under irrigated and rainfed is presented in Figure 2 and Figure 3, respectively. Under irrigated conditions (E1), GY had strong positive and significant correlation with SRM (0.92), BYP (0.73), TGW (0.66), HI (0.56) and negatively associated with D75M (-0.83) whereas in E2 (moisture-stress), GY was significantly positively correlated with GPS (0.92), HI (0.81), TGW (0.71) and negatively correlated with ELWL (-0.92) and D75M (-0.92). Similar associations were also reported by Masood et al. (2014) for HI and BYP with GY under non-stress and moisture-stress environments. Majumder et al. (2008) reported that GPS, TGW and HI were the most important characters having positive association with GY.

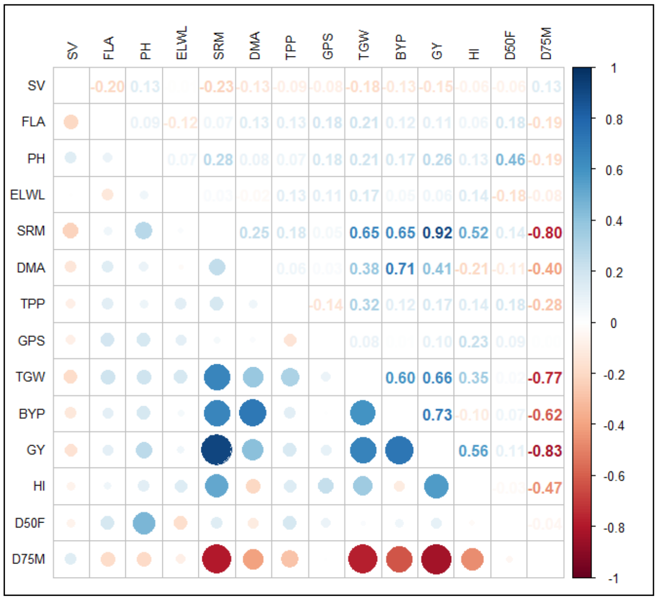

Figure 2: Pearson's correlation coefficients among fourteen traits evaluated under irrigated conditions (E_1)

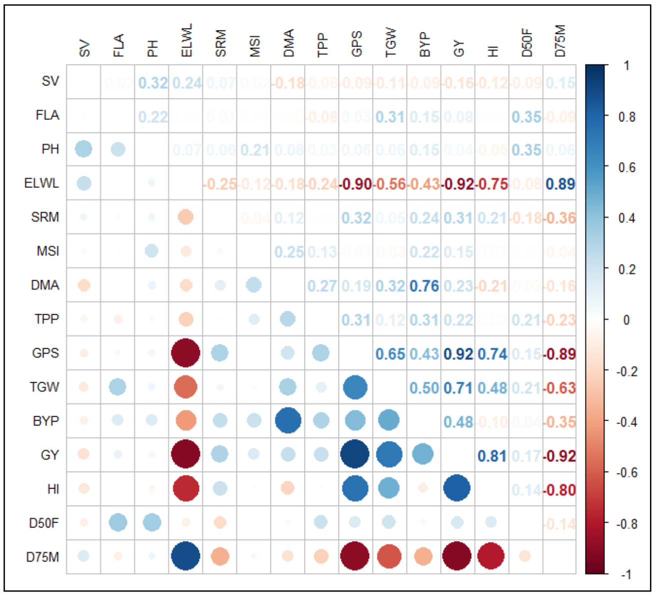

Figure 3: Pearson's correlation coefficients among fourteen traits evaluated under rainfed/moisture stress conditions (E_2)

For other traits like ELWL, no significant associations were found with any of the traits evaluated in E1 while ELWL showed significant associations with GY (-0.92), GPS (-0.90), HI (-0.75), TGW (-0.56) and D75M (0.89). SRM was found to be positively correlated with GY (0.92), TGW (0.65), BYP (0.65), HI (0.52) and negatively correlated with D75M (-0.80) but none of the traits evaluated were associated under moisture stress (E2) conditions. Noorka et al. (2013) found that SRM was an important index of drought resistance and genotypes having higher capacity to mobilize its reserves may be considered to show good performance under drought stress conditions. DMA observed was found to be positively correlated with BYP under both E1 (0.71) and E2 (0.76) conditions. Grains in each spike (GPS) evaluated showed no correlation with any of the traits evaluated in E1 but positive correlation with GY (0.92), HI (0.74), TGW (0.65) and negative association with ELWL (-0.90), D75M (-0.89) in E2. TGW of the genotypes evaluated showed significant positive association with GY (0.66), SRM (0.65), BYP (0.60) and negative correlation with D75M (-0.77) in E1 whereas TGW was positively correlated with GY (0.71), GPS (0.65), BYP (0.50) and negative association with D75M (-0.63), ELWL (-0.56) in E2. BYP showed positive relationship with GY (0.73), DMA (0.71), SRM (0.65), TGW (0.60) and negative association with D75M (-0.62) in E1 whereas positively correlated with DMA (0.76), BYP (0.50) in E2. HI showed significant association with GY (0.56) and SRM (0.52) in E1 while HI was positively correlated with GY (0.81), GPS (0.74) and negatively correlated with ELWL (-0.75) and D75M (-0.80). D75M recorded in E1 showed negative association with GY (-0.83), SRM (-0.80), TGW

(-0.77) and BYP (-0.62) whereas positive association of D75M was observed with ELWL (0.89) and negative association with GY (-0.92), GPS (-0.89), HI (-0.80) and TGW (-0.63). Giriyappanavar et al. (2010) reported that under stressed conditions early maturing genotypes were preferred. Traits viz., SV, FLA, PH, ELWL, TPP, GPS and D50F in E1 while SV, FLA, PH, SRM, MSI, TPP and D50F in E2 had weak associations among all the traits evaluated.

3.5. Genetic divergence

Genetic variability is the basic requirement for making progress in crop breeding. The narrow genetic base of the elite germplasm has increased the potential vulnerability to biotic and abiotic stresses. So, it is mandatory to identify genetically diverse lines for future wheat breeding. Inclusion of genetically diverse parents in any breeding programme is essential to create new genetic stocks and can help in maintain it for long-term selection gains and to develop superior pure lines. D^2 statistics is a powerful tool for estimating genetic diversity among different genotypes and to assess the relative contribution of different components to the total divergence both at inter and intra cluster level. The assessment of genetic diversity helps in reducing the number of breeding lines from the large germplasm and the progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants. Simultaneous test of significance based on Wilk's criterion and D^2 values obtained for each pair of populations were observed to be significant, which indicated presence of sufficient genetic diversity among germplasm lines studied in the present investigation.

The clustering of genotypes based on the pooled mean over three environments formed twelve clusters. Among them, clusters I, II, III and IV were poly-genotypic, whereas rest were mono-genotypic (Figure 4 and Table 5). Cluster I was the largest consisting of seventeen lines viz., CM 19, CM 17, C 306, CM 18, HPW 155, CM 2, CM 23, VL 907, CM 26, HPW 292, HPW 280, NIAW 34, CM 10, HPW 368, HPW 327 and CM 27. Cluster IV was second largest cluster including thirteen lines viz., DPW 621-50, CM 33, HPW 299, HPW 147, HPW 89, HPW 301, HS 507, Bhalyani Collection, CM 11, CM 32, HPW 236, HPW 297 and HPW 277. Genotypes HW 2004, CM 16, HD 2888, CM 29, CM 43, HPW 281, HPW 302, WH 1021 and CM 24 formed cluster II. Whereas, cluster III consisted of NI 5439, HPW 349, HPW 269, CM 15, CM 20, HPW 376, VL 892, HPW 334 and CM 39. However cluster V, VI, VII, VIII, IX, X, XI and XII were formed by genotypes CM 41, CM 42, Kanku, PBW 550, NIAW 1415, WR 544, NIAW 1689 and DBW 17, respectively.

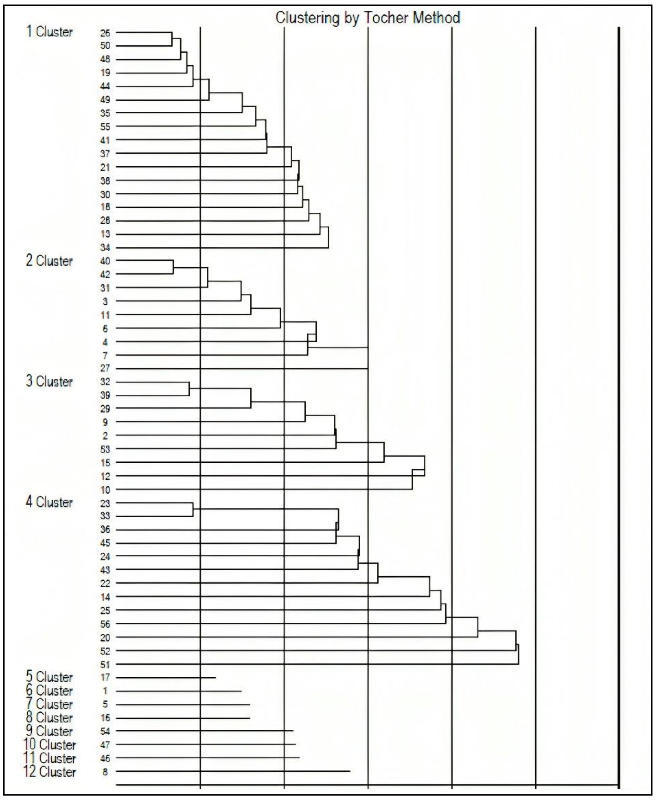

Figure 4: Phenogram of wheat genotypes generated using Mahalanobis D^2 analysis under pooled analysis over three environments

Different clustering pattern were also reported in wheat by earlier workers (Alamerew and Degewione, 2013; Amin et al., 2014). While Khan et al. (2014) grouped 25 genotypes into eight clusters on the basis of D^2 statistic out of which cluster I had maximum number of genotypes.

A perusal of Table 6 based on pooled mean of three environments showed that, cluster IV had the highest intra-cluster distance (2.10) followed by cluster III (1.88) and cluster II (1.59) whereas the highest inter-cluster distance was observed between clusters VII and XII (4.84) followed by clusters VII and X (4.19) and clusters VII and IX (4.11). The distance between cluster V and VI was minimum (1.22) followed by the distance between clusters V and VIII (1.26). Varying intra and inter-cluster distances have also been recorded by earlier researchers on diverse germplasm (Tsegaye et al., 2012; Amin et al., 2014). These results suggested that the genotypes falling in cluster showing highest cluster mean for maximum number of traits can be selected directly on the basis of these traits and used in hybridization programme to get maximum transgressive segregants. The scattering of yield and its component characters in different clusters in the present study showed a lot of scope for hybridization among the genotypes of these clusters. Hence, pooled analysis of genetic divergence

Table 5: Distribution of wheat genotypes among different clusters on the basis of D^2 analysis under pooled analysis over environments

Cluster	No of genotypes	Genotypes
I	17	CM19, CM17, C306, CM18, HPW155, CM2, CM23, VL907, CM26, HPW292, HPW280, NIAW34, HS 490, CM10, HPW368, HPW327, CM27
II	9	HW2004, CM16, HD2888, CM29, CM43, HPW281, HPW302, WH1021, CM24
III	9	NI5439, HPW349, HPW269, CM15, CM20, HPW376, VL892, HPW334, CM39
IV	13	DPW 621-50, CM33, HPW299, HPW147, HPW89, HPW301, HS507, Bhalyani Collection, CM11, CM32, HPW236, HPW297, HPW277
V	1	CM41
VI	1	CM42
VII	1	Kanku
VIII	1	PBW550
IX	1	NIAW1415
X	1	WR544
XI	1	NIAW1689
XII	1	DBW17

Table 6: Average intra and inter cluster values of D^2 and $\sqrt{D^2}$ among clusters under pooled analysis over environments

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	2.19	4.08	3.92	4.12	3.72	5.52	9.24	4.49	3.76	6.66	7.08	7.67
	(1.48)	(2.02)	(1.98)	(2.03)	(1.93)	(2.35)	(3.04)	(2.12)	(1.94)	(2.58)	(2.66)	(2.77)
II	-	2.53	4.45	5.52	6.86	8.58	4.04	7.56	7.73	10.82	5.02	13.47
		(1.59)	(2.11)	(2.35)	(2.62)	(2.93)	(2.01)	(2.75)	2.78	(3.29)	(2.24)	(3.67)
III	-	-	3.53	6.86	4.54	4.80	9.06	5.90	4.37	6.00	6.25	8.94
			(1.88)	(2.62)	(2.13)	(2.19)	(3.01)	(2.43)	(2.09)	(2.45)	(2.50)	(2.99)
IV	-	-	-	4.41	7.56	10.76	11.36	8.01	6.00	12.04	7.78	11.49
				(2.10)	(2.75)	(3.28)	(3.37)	(2.83)	(2.45)	(3.47)	(2.79)	(3.39)
V	-	-	-	-	0.00	1.49	12.74	1.59	3.53	4.16	8.35	3.39
					(0.00)	(1.22)	(3.57)	(1.26)	(1.88)	(2.04)	(2.89)	(1.84)
VI	-	-	-	-	-	0.00	13.91	3.03	4.49	2.13	9.67	3.61
						(0.00)	(3.73)	(1.74)	(2.12)	(1.46)	(3.11)	(1.90)
VII	-	-	-	-	-	-	0.00	13.40	16.89	17.56	8.70	23.43
							(0.00)	(3.66)	(4.11)	(4.19)	(2.95)	(4.84)
VIII	-	-	-	-	-	-	-	0.00	5.20	3.69	6.35	2.79
								(0.00)	(2.28)	(1.92)	(2.52)	(1.67)
IX	-	-	-	-	-	-	-	-	0.00	5.81	7.67	4.37
									(0.00)	(2.41)	(2.77)	(2.09)
X	-	-	-	-	-	-	-	-	-	0.00	11.63	4.93
										(0.00)	(3.41)	(2.22)

Table 6: Continue...

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
XI	-	-	-	-	-	-	-	-	-	-	0.00 (0.00)	10.24 (3.20)
XII	-	-	-	-	-	-	-	-	-	-	-	0.00 (0.00)

Bold values are intra-cluster distance, Data in parenthesis are $\sqrt{D^2}$ value

showed that the plant height (30.65%) followed by seedling vigour (22.99%), flag leaf area (11.10%), biological yield (6.82%) and grain yield plant^{-1} (7.79%) contributed maximum towards genetic divergence (Table 6). Yadav et al. (2014) reported that GY followed by test weight and GPS contributed maximum to genetic divergence and Khan et al. (2014) revealed that GPS, yield plot^{-1} and PH contributed maximum towards divergence.

4. CONCLUSION

Significant variability was observed for almost all the traits evaluated under irrigated and rainfed conditions. Based on low DSI and high DRI values, seven wheat genotypes HPW 368, NI 5439, CM 33, CM 19, HPW 236, CM 11 and HPW 349 were found drought tolerant. Diversity studies categorized wheat population into twelve clusters and three genotypes HPW 277, HPW 297 and NIAW 1415 were found to be superior and diverse for most of the traits evaluated.

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